

Application No.: 10/821,710

2

Docket No.: 546322000304

Amendments to the Specification:

Please amend the paragraph beginning on page 8, line 15 as follows:

—The introduced dispersed nucleic acid molecule or foreign nucleic acid molecule sequence, needing less than absolute homology, also need not be full length, relative to either the primary transcription product or fully processed mRNA of the target gene. A higher homology in a shorter than full length sequence compensates for a longer less homologous sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments will be equally effective. Normally, a sequence of greater than 20-100 nucleotides should be used, though a sequence of greater than about 200-200 nucleotides would be preferred, and a sequence of greater than 500-1000 nucleotides would be especially preferred depending upon the size of the target gene. The nucleotide sequence of each unit may comprise at least about 1 to 200 nucleotides in length and preferred nucleotide sequences are at least about 20 to 30 nucleotides in length.—

sf-1964878